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Score = 619 bits (1580), Expect = e-175
Identities = 300/302 (99%), Positives = 300/302 (99%), Gaps = 0/302 (0%)
Frame = +1

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ACCESSION   NM_198185
VERSION     NM_198185.1  GI:38044105
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Puente,X.S., Sanchez,L.M., Overall,C.M. and Lopez-Otin,C.
  TITLE     Human and mouse proteases: a comparative genomic approach
  JOURNAL   Nat. Rev. Genet. 4 (7), 544-558 (2003)
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Nov 3 2003 07:26:36

Homo sapiens. Human CVSP14 full length cDNA. PA:CORVAS INT INC.
PN:WO200277263-A2. gsn
Length = 1035

Score = 628 bits (1603), Expect = e-179
Identities = 305/306 (99%), Positives = 306/306 (100%), Gaps = 0/306 (0%)
Frame = +1

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Sbjct: 295  QVEKGSYPWQVSLKQRQKHICGGSIVSPQWVITAAHCIANRNIVSTLNVTAGEYDLSQTD 474

Query: 119  PGEQTLTIETVIIHPHFSTKKPMDYDIALLKMAGAFQFGHFVGPICLPELREQFEAGFIC 178
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View Images

## PUBLISHED INTERNATIONAL APPLICATION

(11) **WO 02/*077263*** (13) A2

(21) PCT/US02/09039

(22) **20 March 2002 (20.03.2002)**

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(31) 60/278,166 (32) 22 March 2001 (22.03.2001) US

(43) 03 October 2002 (03.10.2002)

(51)[7] C12Q

(54) NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE CVSP14, THE ENCODED POLYPEPTIDES AND METHODS BASED THEREON

(61) US 60/278,166 (CIP)

Filed on 22 March 2001 (22.03.2001)

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(81)

AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW

(84)

ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)

For information on time limits for entry into the national phase please click here

Published *without international search report and to be republished upon receipt of that report*

Declaration under Rule 4.17 *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)*

*as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)*

No Image Available.

## Abstract

Provided herein are polypeptides designated CVSP14 polypeptides that exhibit protease activity as a single chain or as an activated two chain form. Methods using the polypeptides to identify compounds that modulate the protease activity thereof are provides. The polypeptides also serve as tumor markers.

Homo sapiens. Human protease PRTS-20 cDNA sequence. PA:INCYTE GENOMICS INC.
PN:WO200198468-A2. gsn
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Score = 628 bits (1603), Expect = e-179
Identities = 305/306 (99%), Positives = 305/306 (99%), Gaps = 0/306 (0%)
Frame = +3

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Français

1 of 1

View Images

## PUBLISHED INTERNATIONAL APPLICATION


| | | | | |
|---|---|---|---|---|
| (11) | **WO 01/*98468*** | (13) | A2 | |
| (21) | PCT/US01/19178 | | | |
| (22) | **13 June 2001 (13.06.2001)** | | | |
| (25) | ENG | (26) | ENG | |
| (31) | 60/212,336 | (32) | 16 June 2000 (16.06.2000) | US |
| (31) | 60/213,955 | (32) | 22 June 2000 (22.06.2000) | US |
| (31) | 60/215,396 | (32) | 29 June 2000 (29.06.2000) | US |
| (31) | 60/216,821 | (32) | 07 July 2000 (07.07.2000) | US |
| (31) | 60/218,946 | (32) | 14 July 2000 (14.07.2000) | US |
| (43) | 27 December 2001 (27.12.2001) | | | |
| (51)[7] | C12N 9/00 | | | |
| (54) | PROTEASES | | | |



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Road, Canterbury, Kent CT1 3EZ; (GB) [US/IE].**AZIMZAI, Yalda** 5518 Boulder Canyon Drive, Castro Valley, CA 94552; (US) [US/US].**LU, Yan** 3885 Corrina Way, Palo Alto, CA 94303; (US) [US/CN].**RAMKUMAR, Jayalaxmi** 34359 Maybird Circle, Fremont, CA 94555; (US) [US/IN].**XU, Yuming** 1739 Walnut Drive, Mountain View, CA 94040; (US) [US/US].**REDDY, Roopa** 1233 W. McKinley Avenue #3, Sunnyvale, CA 94086; (US) [US/IN].**DAS, Debopriya** 1179 Bonita Avenue, Apt. 3, Mountain View, CA 94040; (US) [US/IN].**KEARNEY, Liam** 50 Woodside Avenue, San Francisco, CA 94127; (US) [US/IE].**KALLICK, Deborah, A.** 900 Olive Street, Menlo Park, CA 94025; (US) [US/US].

(74) **HAMLET-COX, Diana** Incyte Genomics, Inc., 3160 Porter Drive, Palo Alto, CA 94304; (US).

(81)

AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW

(84)

ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG)

For information on time limits for entry into the national phase please click here

Published *without international search report and to be republished upon receipt of that report*

No Image Available.

## Abstract

The invention provides human proteases (PRTS) and polynucleotides which identify and encode PRTS. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of PRTS.

Français

**Presentation:** Basic **Image:** Small

1 of 1

characterize the protein. A starting material that can only be used to produce a final product does not have a substantial asserted utility in those instances where the final product is not supported by a specific and substantial utility. In this case none of the proteins that are to be produced as final products resulting from processes involving the claimed cDNA have asserted or identified specific and substantial utilities. The research contemplated by Applicants to characterize potential protein products, especially their biological activities, does not constitute a specific and substantial utility. Identifying and studying the properties of the protein itself or the mechanisms in which the protein is involved does not define a "real world" context of use. Note, because the claimed invention is not supported by a specific and substantial asserted utility for the reasons set forth above, credibility has not been assessed. Neither the specification as filed nor any art of record discloses or suggests any property or activity for the cDNA compounds such that another non-asserted utility would be well established for the compounds.

Claim 1 is also rejected under 35 U.S.C. § 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art would not know how to use the claimed invention.

**Example 10: <u>DNA Fragment encoding a Full Open Reading Frame (ORF)</u>**

**Specification:** The specification discloses that a cDNA library was prepared from human kidney epithelial cells and 5000 members of this library were

sequenced and open reading frames were identified. The specification discloses a Table that indicates that one member of the library having SEQ ID NO: 2 has a high level of homology to a DNA ligase. The specification teaches that this complete ORF (SEQ ID NO: 2) encodes SEQ ID NO: 3. An alignment of SEQ ID NO: 3 with known amino acid sequences of DNA ligases indicates that there is a high level of sequence conservation between the various known ligases. The overall level of sequence similarity between SEQ ID NO: 3 and the consensus sequence of the known DNA ligases that are presented in the specification reveals a similarity score of 95%. A search of the prior art confirms that SEQ ID NO: 2 has high homology to DNA Ligase encoding nucleic acids and that the next highest level of homology is to alpha-actin. However, the latter homology is only 50%. Based on the sequence homologies, the specification asserts that SEQ ID NO: 2 encodes a DNA ligase.

**Claim 1:** An isolated and purified nucleic acid comprising SEQ ID NO: 2.

**Analysis:** The following analysis includes the questions that need to be asked according to the guidelines and the answers to those questions based on the above facts:

1) Based on the record, is there a "well established utility" for the claimed invention? Based upon applicant's disclosure and the results of the PTO search, there is no reason to doubt the assertion that SEQ ID NO: 2 encodes a DNA ligase. Further, DNA ligases have a well-established use in the molecular biology art based on this class of protein's ability to ligate DNA. Consequently the answer to the question is yes.

Note that if there is a well-established utility already associated with the claimed invention, the utility need not be asserted in the specification as filed. In order to determine whether the claimed invention has a well-established utility the examiner must determine that the invention has a specific, substantial and credible utility that would have been readily apparent to one of skill in the art. In this case SEQ ID NO: 2 was shown to encode a DNA ligase that the artisan would have recognized as having a specific, substantial and credible utility based on its enzymatic activity.

Thus, the conclusion reached from this analysis is that a 35 U.S.C. § 101 rejection and a 35 U.S.C. § 112, first paragraph, utility rejection should not be made.

**Example 11: Animals with Uncharacterized Human Genes**

**Specification:** Kidney cells from a patient with Polycystic Kidney (PCK) Disease have been used to make a cDNA library. From this library 8000 nucleotide "fragments" have been sequenced but not yet used to express proteins in a transformed host cell nor have they been characterized in any other way. The 50 longest fragments, SEQ ID NO: 1-50, respectively, have been used to make transgenic mice. None of the 50 lines of mice have developed Polycystic Kidney Disease to date. The asserted utility is the use of the mice to research human genes from diseased human kidneys. The disease is inheritable, but chromosomal loci have not yet been identified. Neither the absence or presence of a specific protein has been identified with the disease condition.

**Query=** SEQ ID NO:1
(921 letters)

| Sequences producing significant alignments: | Score (bits) | E Value |
|---|---|---|
| AC104237.2.1.164732 | 391 | e-106 |

>AC104237.2.1.164732
Length = 164732

Score = 391 bits (197), Expect = e-106
Identities = 200/201 (99%)
Strand = Plus / Plus

```
Query: 721   cagggagattcaggaggttcactcatgtgccggaataagaaaggggcctggactctggct 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 51293 cagggagattcaggaggttcactcatgtgccggaataagaaaggggcctggactctggct 51352


Query: 781   ggtgtgacttcctggggtttgggctgtggtcgaggctggagaaacaatgtgaggaaaagt 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 51353 ggtgtgacttcctggggtttgggctgtggtcgaggctggagaaacaatgtgaggaaaagt 51412


Query: 841   gatcaaggatcccctgggatcttcacagacattagtaaagtgctttcctggatccacgaa 900
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct: 51413 gatcaaggatcccctgggatcttcacagacattagtaaagtgcttccctggatccacgaa 51472


Query: 901   cacatccaaactggtaactaa 921
              ||||||||||||||||||||
Sbjct: 51473 cacatccaaactggtaactaa 51493
```

Score = 349 bits (176), Expect = 1e-93
Identities = 176/176 (100%)
Strand = Plus / Plus

```
Query: 301   agaaacattgtgtctactttgaatgttactgctggagagtatgacttaagccagacagac 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 49450 agaaacattgtgtctactttgaatgttactgctggagagtatgacttaagccagacagac 49509


Query: 361   ccaggagagcaaactctcactattgaaactgtcatcatacatccacatttctccaccaag 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 49510 ccaggagagcaaactctcactattgaaactgtcatcatacatccacatttctccaccaag 49569


Query: 421   aaaccaatggactatgatattgccctttgaagatggctggagccttccaatttgg 476
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 49570 aaaccaatggactatgatattgccctttgaagatggctggagccttccaatttgg 49625
```

```
 Score =  308 bits (155), Expect = 5e-81
 Identities = 155/155 (100%)
 Strand = Plus / Plus


Query: 570   aggtggcgtcctctcacaagtcttgcaggaagtgaatctgcctattttgacctgggaaga 629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50304 aggtggcgtcctctcacaagtcttgcaggaagtgaatctgcctattttgacctgggaaga 50363


Query: 630   gtgtgtggcagctctgttaacactaaagaggcccatcagtgggaagacctttctttgcac 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50364 gtgtgtggcagctctgttaacactaaagaggcccatcagtgggaagacctttctttgcac 50423


Query: 690   aggttttcctgatggagggagagacgcatgtcagg 724
              |||||||||||||||||||||||||||||||||
Sbjct: 50424 aggttttcctgatggagggagagacgcatgtcagg 50458



 Score =  226 bits (114), Expect = 2e-56
 Identities = 114/114 (100%)
 Strand = Plus / Plus


Query: 99    agctcccagttgtgggcagagtctggttaaggtacagccttggaattattttaacatttt 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query: 159   cagtcgcattcttggaggaagccaagtggagaagggttcctatccctggcaggt 212
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Sbjct: 47165 cagtcgcattcttggaggaagccaagtggagaagggttcctatccctggcaggt 47218



 Score =  197 bits (99), Expect = 1e-47
 Identities = 99/99 (100%)
 Strand = Plus / Plus


Query: 475   ggccactttgtggggcccatatgtcttccagagctgcgggagcaatttgaggctggtttt 534
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Sbjct: 49969 ggccactttgtggggcccatatgtcttccagagctgcgggagcaatttgaggctggtttt 50028


Query: 535   atttgtacaactgcaggctggggccgcttaactgaaggt 573
              |||||||||||||||||||||||||||||||||||||
Sbjct: 50029 atttgtacaactgcaggctggggccgcttaactgaaggt 50067
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Score = 191 bits (96), Expect = 9e-46
Identities = 98/100 (98%)
Strand = Plus / Plus

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Query: 1     atgagtctcaaaatgcttataagcaggaacaagctgattttactactaggaatagtcttt 60
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Sbjct: 45375 atgagtctcaaaatgcttataagcaggaacaagctgattttactactaggaatagtcttt 45434


Query: 61    tttgaacraggtaaatctgcarctctttcgctccccaaag 100
              ||||||| |||||||||||| ||||||||||||||||||
Sbjct: 45435 tttgaacgaggtaaatctgcaactctttcgctccccaaag 45474
```

Score = 187 bits (94), Expect = 1e-44
Identities = 94/94 (100%)
Strand = Plus / Plus

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Query: 209   aggtatctctgaaacaaaggcagaagcatatttgtggaggaagcatcgtctcaccacagt 268
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Sbjct: 47990 aggtatctctgaaacaaaggcagaagcatatttgtggaggaagcatcgtctcaccacagt 48049


Query: 269   gggtgatcacggcggctcactgcattgcaaacag 302
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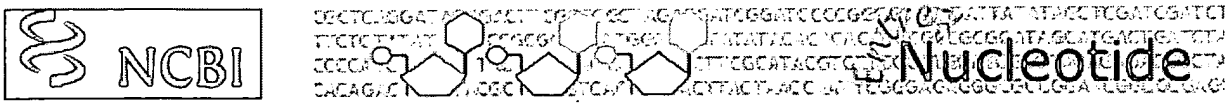




☐ 1: AC104237. Homo sapiens chro...[gi:20128277] Links

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LOCUS       AC104237               164732 bp    DNA     linear   PRI 30-APR-2002
DEFINITION  Homo sapiens chromosome 11, clone RP11-35J10, complete sequence.
ACCESSION   AC104237
VERSION     AC104237.2  GI:20128277
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 164732)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 11, clone RP11-35J10
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 164732)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
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  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 164732)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
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